



|         |            |               |        |           |      |                 |       |         |
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☐ 1: AAC62840. R33083\_1 [Homo sa...[gi:3702295]

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LOCUS AAC62840 432 aa linear PRI 05-OCT-1998  
 DEFINITION R33083\_1 [Homo sapiens].  
 ACCESSION AAC62840  
 VERSION AAC62840.1 GI:3702295  
 DBSOURCE locus AC005783 accession AC005783.1  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (residues 1 to 432)  
 AUTHORS Lamerdin, J.E., McCreedy, P.M., Skowronski, E., Viswanathan, V.,  
 Burkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S.,  
 Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J.,  
 Danganan, L., Erler, A., Christensen, M., Georgescu, A., Avila, J.,  
 Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G.,  
 Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G.,  
 Kronmiller, B., Arellano, A., Saunders, C., Ow, D., Nolan, M., Trong, S.,  
 Kobayashi, A., Olsen, A.S. and Carrano, A.V.  
 TITLE Sequence analysis of a 2.5 Mb region in 19p13.3  
 JOURNAL Unpublished  
 REFERENCE 2 (residues 1 to 432)  
 AUTHORS Lamerdin, J.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-OCT-1998) Joint Genome Institute, Lawrence Livermore  
 National Laboratory, 7000 East Ave., Livermore, CA 94551, USA  
 COMMENT Method: conceptual translation supplied by author.  
 FEATURES Location/Qualifiers

source

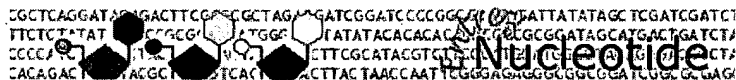
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 /cell\_line="5HL2-B"  
 /clone\_lib="LL19NC03 R chromosome 19-specific cosmid library"  
 /note="Cosmid library constructed at LLNL from flow-sorted chromosomes from human-hamster hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."

Protein

1..>432  
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 /name="Hypothetical partial human protein most similar to Caenorhabditis elegans ORF encoded by (AF043699) contains similarity to the"

CDS

1..432  
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 /note="Should represent 5'-end of hypothetical protein"



1: AC005783. Homo sapiens chro...[gi:3702294] [Links](#)

CDS

similarity to the; Should represent 5'-end of hypothetical protein R26894\_1 encoded by AC005594. Predicted primarily on basis of Xgrail and BLAST similarities"

~~/codon\_start=1~~

/evidence=not\_experimental

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/protein\_id="AAC62840.1"

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repeat region

424..765

/rpt\_family="MLT1B"

repeat region

1161..1457

/rpt\_family="AluJb"

repeat region

1568..1869

/rpt\_family="AluY"

misc feature

complement(2907..2968)

/note="predicted exon, program: grail2exons\_human\_1.3,  
frame: 2, quality: excellent, score: 100.000"

repeat region

3603..3664

/rpt\_family="MIR"

repeat region

3878..4178

/rpt\_family="AluJo"

repeat region

complement(4200..4518)

/rpt\_family="MER58B"

misc feature

complement(4718..4871)

/note="predicted exon, program: grail2exons\_human\_1.3,  
frame: 2, quality: excellent, score: 98.000"

repeat region

4965..5045

/rpt\_family="MIR"

misc feature

complement(5294..5407)

/note="predicted exon, program: grail2exons\_human\_1.3,  
frame: 2, quality: excellent, score: 100.000"

repeat region

5481..5563

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repeat region

complement(5586..5765)

/rpt\_family="MER20"

repeat region

6034..6305

/rpt\_family="AluSq"

misc feature

complement(6577..6745)

/note="predicted exon, program: grail2exons\_human\_1.3,  
frame: 0, quality: excellent, score: 100.000"

misc feature

complement(6801..6995)

/note="predicted exon, program: grail2exons\_human\_1.3,  
frame: 2, quality: excellent, score: 100.000"

misc feature

complement(7099..7216)

/note="predicted exon, program: grail2exons\_human\_1.3,  
frame: 0, quality: good, score: 53.000"

repeat region

7434..7704

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repeat region

complement(7921..8174)

/rpt\_family="AluJo"

misc feature

complement(8549..8661)

/note="predicted exon, program: grail2exons\_human\_1.3,  
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repeat region

8906..9038

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repeat region

9041..9107

/rpt\_family="(GAAA)n"

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                /rpt_family="MER20"
repeat region 9764..9852
                /rpt_family="MIR"
repeat region complement(10315..10616)
                /rpt_family="AluSx"
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                /rpt_family="L1PA12"
repeat region complement(11616..11908)
                /rpt_family="AluSg"
repeat region 12237..12484
                /rpt_family="L1MB7"
repeat region 14005..14181
                /rpt_family="MLT1C"
repeat region 14182..14483
                /rpt_family="AluSx"
repeat region 14499..14718
                /rpt_family="MLT1C"
repeat region 14960..15260
                /rpt_family="AluJo"
repeat region 15717..15900
                /rpt_family="MER20"
misc feature complement(16772..17028)
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                frame: 2, quality: excellent, score: 100.000"
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                /rpt_family="LINE2"
repeat region complement(17718..18013)
                /rpt_family="AluSq"
repeat region 18187..18271
                /rpt_family="LINE2"
repeat region 19047..19347
                /rpt_family="AluY"
repeat region complement(19410..19515)
                /rpt_family="MIR"
repeat region complement(20778..20911)
                /rpt_family="FLAM_C"
repeat region 21752..22037
                /rpt_family="AluSg"
repeat region 22038..22061
                /rpt_family="(TAA)n"
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                /rpt_family="MER20"
misc feature 22574..22678
                /note="predicted exon, program: grail2exons_human_1.3,
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                /rpt_family="MER20"
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                /rpt_family="MER20"
repeat region 23946..24060
                /rpt_family="LINE2"
repeat region 24191..24485
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repeat region 24575..24797
                /rpt_family="MIR"
repeat region complement(25744..25782)
                /rpt_family="tRNA-Gly-GGA"
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misc feature /rpt\_family="GC\_rich"  
complement(26579..26852)  
/note="BLASTN similarity to X64281 (1005..1279); match: 0.99, score: 2.6e-95; database searched: nt; H.sapiens variant gene for tRNA-Val (anticodon:CAC) and tRNA-Gly (anticodon:UCC) "  
repeat region complement(26589..26625)  
/rpt\_family="GC\_rich"  
repeat region 26761..26832  
/rpt\_family="tRNA-Gly-GGA"  
repeat region complement(26860..27051)  
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repeat region 27052..27087  
/rpt\_family="POLY\_G"  
repeat region complement(27088..27187)  
/rpt\_family="AluSx"  
misc feature complement(27206..27774)  
/note="BLASTN similarity to X17515 (82..650); match: 0.99, score: 2.4e-234; database searched: nt; Human gene for variant cytoplasmic tRNA-Val(CAC)~BLASTN similarity to X64281 (82..650); match: 1, score: 1.9e-234; database searched: nt; H.sapiens variant gene for tRNA-Val (anticodon:CAC) and tRNA-Gly (anticodon:UCC) "  
misc feature 27206..27418  
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misc feature complement(27206..27418)  
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misc feature complement(27773..27788)  
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repeat region 30727..30758  
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repeat region /rpt\_family="AluSq"  
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complement(31800..32097)  
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repeat region /rpt\_family="AluSx"  
32531..33133  
repeat region /rpt\_family="LINE2"  
33136..33426  
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repeat region /rpt\_family="AluSx"  
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repeat region /rpt\_family="AluSx"  
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complement(38939..39092)  
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BASE COUNT 10740 a 11580 c 11888 g 9293 t

ORIGIN

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43501 c
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Revised: July 5, 2002.

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